

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Nov 02 15:14:02 EDT 2007

=====

Application No: 10588425 Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-02 15:01:42.351
Finished: 2007-11-02 15:01:42.609
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 258 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 4
Actual SeqID Count: 4

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)

SEQUENCE LISTING

<110> Zankel, et al.

<120> MANUFACTURE OF HIGHLY PHOSPHORYLATED LYSOSOMAL ENZYMES AND USES THEREOF

<130> 30610/39385A

<140> 10588425

<141> 2007-11-02

<150> US 60/542,586

<151> 2004-02-06

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 2847

<212> DNA

<213> Mus musculus

<400> 1

```

atgaaaggggt ccctcctgct gctgctggtg tcaaacctgc tcctgtgcca gagcgggtcc      60
ggagccgggg cccacatcct actccatgat ttctgctggg ttccccgaga gctgagtggc      120
tcctcccag tcctggagga gactcaccca gctcaccagc agggagccag cagaccaggg      180
ccccgggatg cccaggcaca ccccgccctg cccagagcag tgcccacaca gtgcgacgtc      240
cccccaaca gccgcttcga ttgcgccct gacaaggcca tcaccagga acagtgcgag      300
gcccgcgggt gctgctacat ccctgcaaag caggggctgc agggagccca gatggggcag      360
ccctggtgct tcttcccacc cagctacccc agctacaagc tggagaacct gagctcctct      420
gaaatgggct acacggccac cctgaccctg accaccccca ccttcttccc caaggacatc      480
ctgaccctgc ggctggacgt gatgatggag actgagaacc gcctccaact cagatcaaaa      540
gatccagcta acaggcgcta cgagggtgcc ttggagacct cgcgtgtcca cagccgggca      600
ccgtccccac tctacagcgt ggagttctcc gaggagccct tcggggtgat cgtgcaccgg      660
cagctggacg gccgcgtgct gctgaacacg acggtggcgc ccctgttctt tgcggaccag      720
ttcttccagc tgtccacctc gctgccctcg cagtatatca caggcctcgc cgagcacctc      780
agtcccctga tgctcagcac cagctggacc aggatcacc tgtggaaccg ggaccttgcg      840
cccacgcccg gtgcgaacct ctacgggtct caccctttct acctggcgct ggaggacggc      900
gggtcggcac acggggtgtt cctgctaaac agcaatgcc tggatgtggt cctgcagccg      960

```

agccctgccc ttagctggag gtcgacaggt gggatcctgg atgtctacat cttcctgggc	1020
ccagagccca agagcgtggt gcagcagtac ctggacgttg tgggataccc gttcatgccg	1080
ccatactggg gcctgggctt ccacctgtgc cgctggggct actcctccac cgctatcacc	1140
cgccaggtgg tggagaacat gaccagggcc cacttcccc tggacgtcca atggaacgac	1200
ctggactaca tggactcccg gagggacttc acgttcaaca aggatggctt ccgggacttc	1260
ccggccatgg tgcaggagct gcaccagggc ggccggcgct acatgatgat cgtggatcct	1320
gccatcagca gctcggggcc tgcggggagc tacaggccct acgacgaggg tctgcggagg	1380
ggggttttca tcaccaacga gaccggccag ccgctgattg ggaaggtatg gcccggtcc	1440
actgccttcc ccgacttcac caaccccaca gccctggcct ggtgggagga catggtggct	1500
gagttccatg accaggtgcc cttcgacggc ttgtggattg acatgaacga gccttccaac	1560
ttcatcagag gctctgagga cggtgcccc aacaatgagc tggagaacct accctacgtg	1620
cctgggggtg ttggggggac cctccaggcg gccaccatct gtgcctccag ccaccagttt	1680
ctctccacac actacaacct gcacaacctc tacggcctga ccgaacctat cgctccac	1740
agggcgctgg tgaaggctcg ggggacacgc ccatttgtga tctcccgctc gacctttgct	1800
ggccacggcc gatacgccgg ccaactggacg ggggacgtgt ggagctcctg ggagcagctc	1860
gcctcctccg tgcagaaat cctgcagttt aacctgctgg gggcgctctt ggtcggggcc	1920
gacgtctgcg gcttctctgg caacacctca gaggagctgt gtgtgcgctg gaccagctg	1980
ggggccttct accccttcat gcggaaccac aacagcctgc tcagtctgcc ccaggagccg	2040
tacagcttca gcgagccggc ccagcaggcc atgaggaagg ccctcaccct gcgctacgca	2100
ctctccccc acctctacac actgttccac caggcccacg tcgcggggga gaccgtggcc	2160
cggccctct tcttgagtt ccccaaggac tctagcacct ggactgtgga ccaccagctc	2220
ctgtgggggg aggccttgct catcacccca gtgctccagg ccgggaaggc cgaagtgact	2280
ggctacttcc ccttgggcac atggtacgac ctgcagacgg tgccaataga ggcccttggc	2340
agcctccac cccacctgc agctccccgt gagccagcca tccacagcga ggggcagtgg	2400
gtgacgctgc cggccccct ggacaccatc aacgtccacc tccgggctgg gtacatcatc	2460
ccctgcagg gccctggcct cacaaccaca gagtccgccc agcagcccat ggcctggct	2520
gtggccctaa ccaagggtgg agaggcccga ggggagctgt tctgggacga tggagagagc	2580
ctggaagtgc tggagcgagg ggctacaca caggteatct tcctggccag gaataacacg	2640
atcgtgaatg agctggtacg tgtgaccagt gagggagctg gcctgcagct gcagaaggtg	2700

actgtcctgg gcgtggccac ggcgccccag caggtcctct ccaacggtgt ccctgtctcc 2760

aacttcacct acagccccga caccaaggtc ctggacatct gtgtctcgct gttgatggga 2820

gagcagtttc tcgtcagctg gtgttga 2847

<210> 2

<211> 948

<212> PRT

<213> Mus musculus

<400> 2

Met Lys Gly Ser Leu Leu Leu Leu Leu Val Ser Asn Leu Leu Leu Cys

1 5 10 15

Gln Ser Gly Ser Gly Ala Gly Ala His Ile Leu Leu His Asp Phe Leu

20 25 30

Leu Val Pro Arg Glu Leu Ser Gly Ser Ser Pro Val Leu Glu Glu Thr

35 40 45

His Pro Ala His Gln Gln Gly Ala Ser Arg Pro Gly Pro Arg Asp Ala

50 55 60

Gln Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr Gln Cys Asp Val

65 70 75 80

Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys Ala Ile Thr Gln

85 90 95

Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro Ala Lys Gln Gly

100 105 110

Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe Phe Pro Pro Ser

115 120 125

Tyr Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser Glu Met Gly Tyr

130 135 140

Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe Pro Lys Asp Ile

145 150 155 160

Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu Asn Arg Leu His

165 170 175

Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu Val Pro Leu Glu
180 185 190

Thr Pro Arg Val His Ser Arg Ala Pro Ser Pro Leu Tyr Ser Val Glu
195 200 205

Phe Ser Glu Glu Pro Phe Gly Val Ile Val His Arg Gln Leu Asp Gly
210 215 220

Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe Phe Ala Asp Gln
225 230 235 240

Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr Ile Thr Gly Leu
245 250 255

Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser Trp Thr Arg Ile
260 265 270

Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly Ala Asn Leu Tyr
275 280 285

Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly Gly Ser Ala His
290 295 300

Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val Val Leu Gln Pro
305 310 315 320

Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile Leu Asp Val Tyr
325 330 335

Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln Gln Tyr Leu Asp
340 345 350

Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly Leu Gly Phe His
355 360 365

Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr Arg Gln Val Val
370 375 380

Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val Gln Trp Asn Asp
385 390 395 400

Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe Asn Lys Asp Gly
 405 410 415

Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His Gln Gly Gly Arg
 420 425 430

Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser Ser Gly Pro Ala
 435 440 445

Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg Gly Val Phe Ile
 450 455 460

Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val Trp Pro Gly Ser
 465 470 475 480

Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu Ala Trp Trp Glu
 485 490 495

Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe Asp Gly Leu Trp
 500 505 510

Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly Ser Glu Asp Gly
 515 520 525

Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val Pro Gly Val Val
 530 535 540

Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser Ser His Gln Phe
 545 550 555 560

Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly Leu Thr Glu Pro
 565 570 575

Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly Thr Arg Pro Phe
 580 585 590

Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg Tyr Ala Gly His
 595 600 605

Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu Ala Ser Ser Val
 610 615 620

Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro Leu Val Gly Ala
625 630 635 640

Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu Leu Cys Val Arg
645 650 655

Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg Asn His Asn Ser
660 665 670

Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser Glu Pro Ala Gln
675 680 685

Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala Leu Leu Pro His
690 695 700

Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly Glu Thr Val Ala
705 710 715 720

Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser Thr Trp Thr Val
725 730 735

Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile Thr Pro Val Leu
740 745 750

Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp
755 760 765

Tyr Asp Leu Gln Thr Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro
770 775 780

Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp
785 790 795 800

Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala
805 810 815

Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser
820 825 830

Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu
835 840 845

Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val Leu

850

855

860

Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn Asn Thr
865 870 875 880

Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala Gly Leu Gln
885 890 895

Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala Pro Gln Gln Val
900 905 910

Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr Ser Pro Asp Thr
915 920 925

Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly Glu Gln Phe Leu
930 935 940

Val Ser Trp Cys
945

<210> 3
<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 3
gcgataggta ccgccatggg agtgaggcac ccgccctgct ccc

43

<210> 4
<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer

<400> 4
gcgatactcg agtcaacacc agctgacgag aaactgctct ccc

43